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>gb|EAW85671.1|  BAI1-associated protein 3, isoform CRA_b [Homo sapiens]
Length=1169

Score = 24.8 bits (51), Expect = 586
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query	2	ELLRKKV	8
		ELLRKKV	
Sbjct	764	ELLRKKV	770

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Query 65 KDVV-----DITDELRRRLRGAKGKSVCKICK-KIMLEIAVSKASVVATGECGMDT 114
 K +V +I D + + + C IC KI + + +A + G D
 Sbjct 62 KHIVYDMRETFKTEIIDYFVEEYKQGRTPNPCFICNSKIKFGLFLEQAL-----KDGFDK 116

Query 115 IAGAVLDVSRRTGIEPEFVQLPKRYFNGDDRIIVR 149
 IA TG + ++ K GD+R ++R
 Sbjct 117 IA-----TG---HYAKIEKTEIEGDERFLLR 139

>ref|ZP_01778173.1| tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
 [Petrotoga mobilis SJ95]
 gb|EDJ82392.1| tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
 [Petrotoga mobilis SJ95]
 Length=367

Score = 37.7 bits (86), Expect = 0.70, Method: Composition-based stats.
 Identities = 37/131 (28%), Positives = 61/131 (46%), Gaps = 30/131 (22%)

Query 8 VSGKKICVLISGGMDSAVATKILQLSNTDVRGLH---ITHRWMWFTPEI----- 53
 +S KK+ +L+SGG+DS+VA +L+ N V GLH ++ PE
 Sbjct 1 MSNKKVLMMLMSGGVDSSVAAAYLLKEQNYHVGILHFKTVSDVVFSLIPEKKKVVCCSPSDTQ 60

Query 54 EIKRISKMLGIKD--VVDITDELRRRL-----RGAKGKSVCKICKKIM-----LEIA 98
 + +I+ L + D +VDI E + ++ + K + C +C + LEIA
 Sbjct 61 DALKIADKLDLDDFQIVDIKKEFKEKIIDYFIKTYKEGKTPNPCMLCNRFKFGKALEIA 120

Query 99 VS-KASVVATG 108
 S A V++G
 Sbjct 121 HSYGADWVSSG 131

>ref|ZP_00144111.1| tRNA (5-methylaminomethyl-2-thiouridylate) -methyltransferase
 [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
 gb|EAA24275.1| tRNA (5-methylaminomethyl-2-thiouridylate) -methyltransferase
 [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
 Length=362

Score = 37.4 bits (85), Expect = 0.85, Method: Composition-based stats.
 Identities = 42/181 (23%), Positives = 87/181 (48%), Gaps = 30/181 (16%)

Query 9 SGKKICVLISGGMDSAVATKILQLSNTDVRGLHITHRWMWFTPEIEIKRISKMLGIKD-V 67
 S K+ V +SGG+DS+ +L+ D+ G+ + + + + K++ LGI+ V
 Sbjct 22 SNIKVGVMMSGGVDSSSTVAYLLKQQGYDIFGVMTK---TFKDESDAKKVCDDLGEHYV 78

Query 68 VDTDELRRRL-----RGAKGKSVCKICKK-----IMLEIAVSK-ASVVATGECGMD 113
 +D+ +E + ++ + + C +C + ML+ +SK AS +ATG
 Sbjct 79 LDVRNEFKEKVMDFVNEYMNGRTPNPCMVNCRHIKFGKMLDFILSKGASFMATGH--YT 136

Query 114 TIAGAVLDVSRRTGIEPEFV--QLFKRYFNGDDRI--IVRPLIRIHESDVKRLARLLGVK 169
 + +L V + + + Q+ K DR+ I+ P+ + ++ ++ LA+ +GV+
 Sbjct 137 KLKNGLLSVGDDSNKDQVYFLSQIEK-----DRLSKIIFPVGDLKTKLRELAKQMGRV 190

Query 170 V 170
 V
 Sbjct 191 V 191

>ref|NP_956881.1| **UG** guanine monophosphate synthetase [Danio rerio]
 gb|AAH56730.1| **UG** Guanine monophosphate synthetase [Danio rerio]
 Length=359

Score = 37.4 bits (85), Expect = 0.87, Method: Composition-based stats.
 Identities = 23/64 (35%), Positives = 35/64 (54%), Gaps = 2/64 (3%)

Query 4 LRKKVSGKKICVLISGGMDSAVATKILQ--LSNTDVRGLHITHRWMWFTPEIEIKRISK 61
 +R+KV K+ VL+SGG+DS V T +L L+ V +HI + +M ++
 Sbjct 229 IREKVDKSKVLVLLSGGVDSSTVCTALLNKALNQEQVIAVHIDNGFMRKRESQSVEEALTK 288

Query 62 LGIK 65
 LGIK
 Sbjct 289 LGIK 292

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>ref|ZP_01675115.1| tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
[Candidatus Desulfococcus oleovorans Hxd3]
gb|EAX53590.1| tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
[Candidatus Desulfococcus oleovorans Hxd3]
Length=358

Score = 37.0 bits (84), Expect = 1.0, Method: Composition-based stats.
Identities = 20/55 (36%), Positives = 29/55 (52%), Gaps = 3/55 (5%)

Query 13 ICVLISGGMDSAVATKILQLSNTDVRGLHITHRWMWFTPEIEIKRISKMLGIKDV 67
I VL+SGG+DS VA +L+ S DV +H + PE R+ K+ D+
Sbjct 19 IAVLVSGGIDSLVAAHLLKQSGADVTAIHFL---TGYEPEDRAGRLEKLFTQMDI 70

>ref|YP_388864.1| G hypothetical protein Dde_2372 [Desulfovibrio desulfuricans G
gb|ABB39169.1| G conserved hypothetical protein [Desulfovibrio desulfuricans G2
Length=357

Score = 37.0 bits (84), Expect = 1.1, Method: Composition-based stats.
Identities = 28/87 (32%), Positives = 44/87 (50%), Gaps = 9/87 (10%)

Query 16 LISGGMDSAVATKILQLSNTDVRGLHITHRWMWFTPEIEIKRISKMLGIK-DVVDITDEL 74
L+SGG+DS +A K++Q V+ LH +F E+ R M/G+ VVD++D+
Sbjct 14 LLSGGLDSILAVKVVQEQGLRVKCLHFVTP--FFGKPREVNRWESMGLDIAVVDVSDDF 71

Query 75 RRRLRG-----AKGKSVCKICKKIML 95
+RG K + C CK +M+
Sbjct 72 VSMRGRPAHGYGKVLNPCVDCKILMM 98

>ref|NP_602720.1| G tRNA (5-methylaminomethyl-2-thiouridylate) -methyltransferase
[Fusobacterium nucleatum subsp. nucleatum ATCC 25586]

gb|AAL94019.1| G tRNA (5-methylaminomethyl-2-thiouridylate) -methyltransferase
[Fusobacterium nucleatum subsp. nucleatum ATCC 25586]
Length=343

Score = 37.0 bits (84), Expect = 1.1, Method: Composition-based stats.
Identities = 36/114 (31%), Positives = 58/114 (50%), Gaps = 16/114 (14%)

Query 11 KKICVLISGGMDSAVATKILQLSNTDVRGLHITHRWMWFTPEIE-IKRISKMLG-IKDVV 68
KK+ + +SGG+DS+V+ +L+ +V G+ + + +IE K++ LG I +VV
Sbjct 2 KKVVGMSGGVDSSVSAYLLKEQGYEVIGITINQHLEENSKDIEDTKKVCCKLGIIEVV 61

Query 69 DITDE-----LRRRLRG---AKGKSVCKICK-----KIMLEIAVS-KASVVATG 108
+I + ++ L G K S C I C KI+ +IA A VATG
Sbjct 62 NIRKDFENIVIKYFLEGYN SGKTPSPCIICDDEIKFKILFDIADKYNAEYVATG 115

>ref|ZP_01511681.1| PP-loop [Burkholderia phytofirmans PsJN]
gb|EAV03756.1| PP-loop [Burkholderia phytofirmans PsJN]
Length=336

Score = 37.0 bits (84), Expect = 1.2, Method: Composition-based stats.
Identities = 44/175 (25%), Positives = 80/175 (45%), Gaps = 28/175 (16%)

Query 9 SGKKICVLISGGMDSAVATKILQL-----SNTDVRGLHITHRWMWFTPEIEIKRISKML 62
+G K+ V +SGG DS +IL N D+ +++ + F PE + K L
Sbjct 66 NGDKVMVCLSGGKDSYAMLEIFLMRLRERAPINFDIVAVNLDQKQPGF-PEHVLPEYLKQL 124

Query 63 GIKDVVDITD--ELRRRLRGAKGKSVCKICKK-----IMLEIAVS-KASVVATGECGMDTI 115
I ++ D + +RL +GK+ C +C + I+ +A A+ +A G D +
Sbjct 125 DIPFHIEHQDTYSIVKRLV-PEGKTTCSLCSRLRRGILYRVAGELGATKIALGHHRDDIL 183

Query 116 AGAVLDV---SRRTGIEPEFVQLPKRYFNGDD--RIIVRPLIRIHESDVKRLARL 165
+L++ + G+ P+ DD I++RPL + E+D+++ A L
Sbjct 184 QTLLLNMFYGGKLGKMPPKL-----QSDDGKNIVIRPLAYVKETDLEKYAEL 230

>ref|YP_012451.1| G hypothetical protein DVU3241 [Desulfovibrio vulgaris subsp.
str. Hildenborough]

ref|YP_965598.1| G PP-loop domain protein [Desulfovibrio vulgaris subsp. vulgaris]

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>ref|NP_988352.1| **G** hypothetical protein MMP1232 [Methanococcus maripaludis S2]
 emb|CAF30788.1| **G** conserved hypothetical protein [Methanococcus maripaludis S2]
 Length=296

Score = 136 bits (342), Expect = 1e-30, Method: Composition-based stats.
 Identities = 90/257 (35%), Positives = 141/257 (54%), Gaps = 27/257 (10%)

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Query 11  KKICVLISGGMDSAVATKILQLSNTDVR-GLHITHRWMWFTPEIEIKRISKMLGIKDVV- 68
          +KI V++SGG DSAV+ I + +V +H H+W W E K+++ + +
Sbjct 39  EKIIIVMLSGGKDSAVSLAIKDLGLNVHLCVHFVHKWSWDISTNEAKKLADRFNVPPIIFP 98

Query 69  DITDELRRRLRGAKGKSVCKICKKIM----LEIA-VSKASVVATGECGMDTIAGAVL--- 120
          DIT+EL ++ +GAKGKS+C+ICK IM ++IA V A ++ TGE ++ IAG V
Sbjct 99  DITEELAKKTQGAKGKSICRICKTIMKARMMDIAKVENAKIIMTGETALEKIAGPVFQYI 158

Query 121 -----DVSRRRTGIE----PEFVQLPKRYFNGDDRI-IVRPLIRIHESDVKRLARLLGVKV 170
          V R+ E E ++PKRY +I RPLIR+ DV L + + +
Sbjct 159 RENNASVVRKDEFELYKKMEITKVPKRY-----KIHFFRPLIRVGHFDVFNLQKYKIDI 213

Query 171 RRVGETGDLRRGRREGCPLQHLDPWVDVTDELMDEVWDVNVEALLVARRLGRRVSVKWP 230
          +RV E G+ REGC LQ+ P ++T EL D+++ +N +A +AR G R S+ P+
Sbjct 214 KRVSEAGNKIGYWREGCCLOQCSPTCELTTELFDDLYKINKKATEIARDCGFRASITLPA 273

Query 231 FRIILEGSPEERRHVAE 247
          I + PEE +++ +
Sbjct 274 KEITV--IPEEEKYLKK 288
  
```

>ref|YP_001096890.1| **G** PP-loop domain protein [Methanococcus maripaludis C5]
 gb|AB034675.1| **G** PP-loop domain protein [Methanococcus maripaludis C5]
 Length=296

Score = 133 bits (335), Expect = 9e-30, Method: Composition-based stats.
 Identities = 88/258 (34%), Positives = 142/258 (55%), Gaps = 27/258 (10%)

```

Query 7  KVSQKICVLISGGMDSAVATKILQLSNTDVR-GLHITHRWMWFTPEIEIKRISKMLGIK 65
          K+ +KI V++SGG DSAV+ + + +V +H H+W W E K+++ I
Sbjct 35  KLKDEKIIIVMLSGGKDSAVSLAVAKELGLNVHLCVHFVHKWSWDISTNEAKKLADRFNIP 94

Query 66  DVV-DITDELRRRLRGAKGKSVCKICKKIM----LEIAVSK-ASVVATGECGMDTIAGAV 119
          + ++T+EL ++ +GAKGKS+C+ICK IM ++IA + A ++ TGE ++ IAG V
Sbjct 95  IIFPNVTEELAKKTQGAKGKSICRICKTIMKARMIDIAKEENAKIIMTGETALEKIAGPV 154

Query 120 L-----DVSRRRTGIE----PEFVQLPKRYFNGDDRI-IVRPLIRIHESDVKRLARLL 166
          +V R+ E E ++PKRY +I RPLIR+ DV L +
Sbjct 155 FQYIRENNTNVKRKDEFELYKKMEITKVPKRY-----KIHFFRPLIRVGHFDVFNLQKYY 209

Query 167 GVKVRRVGETGDLRRGRREGCPLQHLDPWVDVTDELMDEVWDVNVEALLVARRLGRRVSV 226
          + ++RV E G+ REGC LQ+ R ++T EL D+++ +N +A +AR G R S+
Sbjct 210 NIDIKRVSEAGNKIGYWREGCCLOQCSPTCELTTELFDDLYKINKKATEIARENGFRASI 269

Query 227 KWPSFRIILEGSPEERRH 244
          P+ I + PEE ++
Sbjct 270 TLPKEITV--IPEEEKY 285
  
```

>ref|ZP_01702630.1| thiamine biosynthesis protein [Methanococcus vannielii SB]
 gb|EAY51115.1| thiamine biosynthesis protein [Methanococcus vannielii SB]
 Length=299

Score = 131 bits (329), Expect = 5e-29, Method: Composition-based stats.
 Identities = 87/260 (33%), Positives = 141/260 (54%), Gaps = 27/260 (10%)

```

Query 8  VSGKKICVLISGGMDSAVATKILQLSNTDVR-GLHITHRWMWFTPEIEIKRISKMLGIK 66
          ++ +KI V++SGG DSAV+ I + +V +H H W W E K+++ +K
Sbjct 36  LNNEKIVVMLSGGKDSAVSLAIKSLGLNVHLCVHFLHDWSWNISTDEAKKLADRFNVI 95

Query 67  VV-DITDELRRRLRGAKGKSVCKICKKIM----LEIAVSK-ASVVATGECGMDTIAGAVL 120
          + DIT+EL ++ +GAKGKS+C+ICK IM +EIA + A ++ TGE ++ IAG +
Sbjct 96  IFPDITEELLKKTQGAKGKSICRICKTIMKARMVEIAKEENAKIIMTGETALEKIAGPIF 155

Query 121 D-----VSRRRTGIE----PEFVQLPKRYFNGDDRI-IVRPLIRIHESDVKRLARLLG 167
          + + R++ E E ++PKRY +I RPLIR+ D+ L +
  
```

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Sbjct 156 EHIRENNKNIKRKSEQELYSQELTKVPKRY-----KIHFFRPLIRVGHFDIFNLQKYNN 210
 Query 168 VKVRRVGETGDLRRGRREGCPLQHLDPWVDVTDELMDEVWDVNVEALLVARRLGRRVSVK 227
 +++ RV E G+ REGC LQ+ P ++ EL D ++ VN A +AR+ G R S+
 Sbjct 211 LEINRVNEAGNKIGYWREGCSLQYCSPEAMISKELFDNLYVVKLATEIARKNGFRASIV 270
 Query 228 WPSFRIILEGSPEERRHVAE 247
 P I + P + ++A+
 Sbjct 271 LPEKEITV--IPNTKENIAK 288

>ref|NP_248010.1| [G] hypothetical protein MJ1016 [Methanocaldococcus jannaschii D 2661]
 sp|Q58422|Y1016 METJA Hypothetical protein MJ1016
 gb|AAB99022.1| [G] hypothetical protein MJ_1016 [Methanocaldococcus jannaschii DS 2661]
 Length=294

Score = 127 bits (318), Expect = 9e-28, Method: Composition-based stats.
 Identities = 81/243 (33%), Positives = 133/243 (54%), Gaps = 14/243 (5%)

Query 13 ICVLISGGMDSAVATKILQLSNTDVRGL-HITHRWMWFTPEIEIKRISKMLGIKDVV-DI 70
 I V+ SGG DS+ A + + ++ L H HRW W + +++++SK I + +I
 Sbjct 37 IVVMASGGKDSSTAIALAKDLGLNIEYLIHFYHRWSWDVSKKMVEKLSKKFDIPVIFYNI 96
 Query 71 TDELRRRLRGAKGKSVCKICKKIMLEIAVSKAS-----VVATGECGMDTIAGAVLDVSR 125
 TDEL +R +GAKG S+C+ICK IM + AV + ++ TG+ ++ ++GAV++ R
 Sbjct 97 TDELLKRTKGAKGSSICRICKNIMKDKAVDISKEKGIRIIMTGDSALEKVSGAVMNYLRD 156
 Query 126 TGIEP-----EFVQLPKRYFNGDDR--IIVRPLIRIHESDVKRLARLLGVKVRVGETGD 178
 E E +P++Y G D+ + RPLIR+ DV +L +++ R E GD
 Sbjct 157 VYGEVVYNKMELTPVPQKYSKGKDKVEVLFRRPLIRLACEDVLKLMDDYNNIEIERAHEVGD 216
 Query 179 LRRGRREGCPLQHLDPWVDVTDELMDEVWDVNVEALLVARRLGRRVSVKWPSFRIILEGS 238
 REGC LQ+ D + ++L +E++ N A VA++ G R S+K PS +I++
 Sbjct 217 KIGFWREGCCLQYADENALLNEKLFNELYKYNKIATEVAKKHGFRASIKLPSKKIMVVPK 276
 Query 239 PEE 241
 +E
 Sbjct 277 KDE 279

>ref|ZP_01799296.1| conserved hypothetical protein [Methanococcus aeolicus Nanka
 gb|EDK16291.1| conserved hypothetical protein [Methanococcus aeolicus Nankai-3]
 Length=302

Score = 125 bits (314), Expect = 3e-27, Method: Composition-based stats.
 Identities = 82/239 (34%), Positives = 129/239 (53%), Gaps = 17/239 (7%)

Query 11 KKICVLISGGMDSAVATKILQLSNTDVR-GLHITHRWMWFTPEIEIKRISKMLGIKDVV- 68
 K I ++SGG DS+ A + + + D++ +H H+W W P+ ++++I+K + +
 Sbjct 37 KPIIAMLSSGGKDSSTALAMAKDLDLIDIKLAVHFVHKWSWELPKTQVQKITKEYDVPLIFY 96
 Query 69 DITDELRRRLRGAK--GKSVCKICKKIM----LEIAV-SKASVVATGECGMDTIAGAVLD 121
 DITD L +R++G GK++CKICK IM EIA KA + TGE ++ IAG +
 Sbjct 97 DITDVLQRIQGGHSGWGNICKICKTIMKEKIREIAYKEKAYTILTGESALEKIAGPIFQ 156
 Query 122 VSRRTG-----IEPEFVQLPKRYFNGDDRIIVRPLIRIHESDVKRLARLLGVKVRVGET 176
 T + E +PK+Y N RPLIR +D++ L + VK+ RVGE
 Sbjct 157 YVNETYGSYVYSKMELTPVPKRYRNK---FFRPLIRCGCNDIEALQKHYNVVKIERVGEV 213
 Query 177 GDLRRGRREGCPLQHLDPWVDVTDELMDEVWDVNVEALLVARRLGRRVSVKWPSFRIIL 235
 G+ REGC LQ+ + + EL D+++ N +AR+ G R S+K PS +I+
 Sbjct 214 GNKIGYWREGCCLQYCNSDTKLNTLFDLDLYYNNRLTALARKHGFRAIKMPSKEVII 272

>ref|NP_126247.1| [G] hypothetical protein PAB1992 [Pyrococcus abyssi GE5]
 emb|CAB49478.1| [G] Predicted ATPase of the PP-loop superfamily [Pyrococcus abyssi GE5]
 Length=260

Score = 110 bits (274), Expect = 1e-22, Method: Composition-based stats.
 Identities = 86/233 (36%), Positives = 130/233 (55%), Gaps = 22/233 (9%)

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ref ZP_01562555.1	PP-loop [Burkholderia cenocepacia MC0-3] >...	35.0	4.5
ref YP_836621.1	PP-loop domain protein [Burkholderia cenocep...]	35.0	4.5
ref ZP_00980938.1	COG0037: Predicted ATPase of the PP-loop s...	34.7	4.9
ref XP_001357491.1	GA21637-PA [Drosophila pseudoobscura] >gb...	34.7	5.0
ref ZP_01518142.1	PP-loop [Comamonas testosteroni KF-1] >gb ...	34.7	5.2
gb ABK78118.1	tRNA (5-methylaminomethyl-2-thiouridylate) met...	34.7	5.5

Alignments

>ref|NP_614974.1| **G** Predicted ATPase of the PP-loop superfamily implicated in ce cycle control [Methanopyrus kandleri AV19]

gb|AAM02904.1| **G** Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Methanopyrus kandleri AV19]
Length=264

Score = 481 bits (1239), Expect = 1e-134, Method: Composition-based stats.
Identities = 262/264 (99%), Positives = 263/264 (99%), Gaps = 1/264 (0%)




Query	1	LELLRKKVSGKKICVLISGGMDSAVATKILQLSNTDVRGLHITHRWMWFTPEIEIKRISK	60
		+ELLRKKVSGKKICVLISGGMDSAVATKILQLSNTDVRGLHITHRWMWFTPEIEIKRISK	
Sbjct	1	MELLRKKVSGKKICVLISGGMDSAVATKILQLSNTDVRGLHITHRWMWFTPEIEIKRISK	60
Query	61	MLGIK-DVVDITDELRRRLRGAKGKSVCKICKKIMLEIAVSKASVVATGECGMDTIAGAV	119
		MLGIK DVVDITDELRRRLRGAKGKSVCKICKKIMLEIAVSKASVVATGECGMDTIAGAV	
Sbjct	61	MLGIKIDVVDITDELRRRLRGAKGKSVCKICKKIMLEIAVSKASVVATGECGMDTIAGAV	120
Query	120	LDVSRRTGIEPEFVQLPKRYFNGDDRIIVRPLIRIHESDVKRLARLLGVKVRVGETGDL	179
		LDVSRRTGIEPEFVQLPKRYFNGDDRIIVRPLIRIHESDVKRLARLLGVKVRVGETGDL	
Sbjct	121	LDVSRRTGIEPEFVQLPKRYFNGDDRIIVRPLIRIHESDVKRLARLLGVKVRVGETGDL	180
Query	180	RRGRREGCPLQHLDPWVDVTDELMDEVWDVNVEALLVARRLGRRVSVKWPSFRIILEGSP	239
		RRGRREGCPLQHLDPWVDVTDELMDEVWDVNVEALLVARRLGRRVSVKWPSFRIILEGSP	
Sbjct	181	RRGRREGCPLQHLDPWVDVTDELMDEVWDVNVEALLVARRLGRRVSVKWPSFRIILEGSP	240
Query	240	EERRHVAECVWYRWVRAGRPRRYR	263
		EERRHVAECVWYRWVRAGRPRRYR	
Sbjct	241	EERRHVAECVWYRWVRAGRPRRYR	264

>ref|ZP_01800055.1| PP-loop domain protein [Methanococcus maripaludis C7]
gb|EDKT7850.1| PP-loop domain protein [Methanococcus maripaludis C7]
Length=296

Score = 137 bits (344), Expect = 7e-31, Method: Composition-based stats.
Identities = 89/257 (34%), Positives = 141/257 (54%), Gaps = 27/257 (10%)

Query	11	KKICVLISGGMDSAVATKILQLSNTDVR-GLHITHRWMWFTPEIEIKRISKMLGIKDVV-	68
		+KI V++SGG DSAVA I + +V +H H+W W E K+++ + +	
Sbjct	39	EKIVVMLSGGKDSAVALAIAKDLGLNVHLCVHFVHKWSWDISTNEAKKLADRFNVPIIFP	98
Query	69	DITDELRRRLRGAKGKSVCKICKKIM----LEIAVSK-ASVVATGECGMDTIAGAVLDVS	123
		DIT+EL ++ +GAKGKS+C+ICK IM ++IA + A ++ TGE ++ IAG V	
Sbjct	99	DITEELAKKTQGAKGKSICRICTIMKARMIDIAKEENAKIIMTGETALEKIAGPVFQYM	158
Query	124	RRTGIE-----PEFVQLPKRYFNGDDRI-IVRPLIRIHESDVKRLARLLGVKV	170
		R + E ++PKRY +I RPLIR+ DV L + + +	
Sbjct	159	RENNSKLNKDEFELYKKMELTKVPKRY-----KIHFFRPLIRVGHFDVFNLQKHXYKIDI	213
Query	171	RRVGETGDLRRGRREGCPLQHLDPWVDVTDELMDEVWDVNVEALLVARRLGRRVSVKWPS	230
		+RV E G+ REGC LQ+ P ++T EL D+++D+N +A +AR+ G R S+ P+	
Sbjct	214	KRVSEAGNKIGYWREGCCLQYCSPTCELTTELFDDLYDLNKKATEIARKNGFRASITLPT	273
Query	231	FRIILEGSPEERRHVAE	247
		I + PEE +++ +	
Sbjct	274	KEITV--IPEEEKYLKK	288

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   **Protein** [\[Sign In\]](#) [\[Regis\]](#)

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from to Features: ☒ CDD

☐ 1: [EAW85671](#). Reports BAI1-associated p...[gi:119606077][BLink](#), [Conserved Domains](#), [Links](#)Features Sequence

LOCUS EAW85671 1169 aa linear PRI 18-DEC-2006

DEFINITION BAI1-associated protein 3, isoform CRA_b [Homo sapiens].

ACCESSION EAW85671

VERSION EAW85671.1 GI:119606077

DBSOURCE accession [CH471112.2](#)

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 1169)

AUTHORS Venter, J.C., Adams, M.D., Myers, E.W., Li, P.W., Mural, R.J., Sutton, G.G., Smith, H.O., Yandell, M., Evans, C.A., Holt, R.A., Gocayne, J.D., Amanatides, P., Ballew, R.M., Huson, D.H., Wortman, J.R., Zhang, Q., Kodira, C.D., Zheng, X.H., Chen, L., Skupski, M., Subramanian, G., Thomas, P.D., Zhang, J., Gabor Miklos, G.L., Nelson, C., Broder, S., Clark, A.G., Nadeau, J., McKusick, V.A., Zinder, N., Levine, A.J., Roberts, R.J., Simon, M., Slayman, C., Hunkapiller, M., Bolanos, R., Delcher, A., Dew, I., Fasulo, D., Flanigan, M., Florea, L., Halpern, A., Hannenhalli, S., Kravitz, S., Levy, S., Mobarry, C., Reinert, K., Remington, K., Abu-Threideh, J., Beasley, E., Biddick, K., Bonazzi, V., Brandon, R., Cargill, M., Chandramouliswaran, I., Charlab, R., Chaturvedi, K., Deng, Z., Di Francesco, V., Dunn, P., Eilbeck, K., Evangelista, C., Gabrielian, A.E., Gan, W., Ge, W., Gong, F., Gu, Z., Guan, P., Heiman, T.J., Higgins, M.E., Ji, R.R., Ke, Z., Ketchum, K.A., Lai, Z., Lei, Y., Li, Z., Li, J., Liang, Y., Lin, X., Lu, F., Merkulov, G.V., Milshina, N., Moore, H.M., Naik, A.K., Narayan, V.A., Neelam, B., Nusskern, D., Rusch, D.B., Salzberg, S., Shao, W., Shue, B., Sun, J., Wang, Z., Wang, A., Wang, X., Wang, J., Wei, M., Wides, R., Xiao, C., Yan, C., Yao, A., Ye, J., Zhan, M., Zhang, W., Zhang, H., Zhao, Q., Zheng, L., Zhong, F., Zhong, W., Zhu, S., Zhao, S., Gilbert, D., Baumhueter, S., Spier, G., Carter, C., Cravchik, A., Woodage, T., Ali, F., An, H., Awe, A., Baldwin, D., Baden, H., Barnstead, M., Barrow, I., Beeson, K., Busam, D., Carver, A., Center, A., Cheng, M.L., Curry, L., Danaher, S., Davenport, L., Desilets, R., Dietz, S., Dodson, K., Doup, L., Ferreira, S., Garg, N., Gluecksmann, A., Hart, B., Haynes, J., Haynes, C., Heiner, C., Hladun, S., Hostin, D., Houck, J., Howland, T., Ibegwam, C., Johnson, J., Kalush, F., Kline, L., Koduru, S., Love, A., Mann, F., May, D., McCawley, S., McIntosh, T., McMullen, I., Moy, M., Moy, L., Murphy, B., Nelson, K., Pfannkoch, C., Pratt, E., Puri, V., Qureshi, H.,

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Reardon,M., Rodriguez,R., Rogers,Y.H., Romblad,D., Ruhfel,B.,
 Scott,R., Sitter,C., Smallwood,M., Stewart,E., Strong,R., Suh,E.,
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 Sato,S., Bafna,V., Istrail,S., Lippert,R., Schwartz,R., Walenz,B.,
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 Levitsky,A., Lewis,M., Liu,X., Lopez,J., Ma,D., Majoros,W.,
 McDaniel,J., Murphy,S., Newman,M., Nguyen,T., Nguyen,N., Nodell,M.,
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 Simpson,M., Smith,T., Sprague,A., Stockwell,T., Turner,R.,
 Venter,E., Wang,M., Wen,M., Wu,D., Wu,M., Xia,A., Zandieh,A. and
 Zhu,X.

TITLE The sequence of the human genome
 JOURNAL Science 291 (5507), 1304-1351 (2001)
 PUBMED 11181995
 REFERENCE 2 (residues 1 to 1169)
 AUTHORS Mural,R.J., Istrail,S., Sutton,G., Florea,L., Halpern,A.L.,
 Mobarry,C.M., Lippert,R., Walenz,B., Shatkay,H., Dew,I.,
 Miller,J.R., Flanigan,M.J., Edwards,N.J., Bolanos,R., Fasulo,D.,
 Halldorsson,B.V., Hannenhalli,S., Turner,R., Yooseph,S., Lu,F.,
 Nusskern,D.R., Shue,B.C., Zheng,X.H., Zhong,F., Delcher,A.L.,
 Huson,D.H., Kravitz,S.A., Mouchard,L., Reinert,K., Remington,K.A.,
 Clark,A.G., Waterman,M.S., Eichler,E.E., Adams,M.D.,
 Hunkapiller,M.W., Myers,E.W. and Venter,J.C.

TITLE Direct Submission
 JOURNAL Submitted (05-JUL-2005) Celera Genomics, 45 W. Gude Dr., Rockville,
 MD 20850, USA
 REFERENCE 3 (residues 1 to 1169)
 AUTHORS Mural,R.J., Istrail,S., Sutton,G., Florea,L., Halpern,A.L.,
 Mobarry,C.M., Lippert,R., Walenz,B., Shatkay,H., Dew,I.,
 Miller,J.R., Flanigan,M.J., Edwards,N.J., Bolanos,R., Fasulo,D.,
 Halldorsson,B.V., Hannenhalli,S., Turner,R., Yooseph,S., Lu,F.,
 Nusskern,D.R., Shue,B.C., Zheng,X.H., Zhong,F., Delcher,A.L.,
 Huson,D.H., Kravitz,S.A., Mouchard,L., Reinert,K., Remington,K.A.,
 Clark,A.G., Waterman,M.S., Eichler,E.E., Adams,M.D.,
 Hunkapiller,M.W., Myers,E.W. and Venter,J.C.

TITLE Direct Submission
 JOURNAL Submitted (02-SEP-2005) Celera Genomics, 45 W. Gude Dr., Rockville,
 MD 20850, USA

COMMENT Method: conceptual translation.

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 Ca2+-binding motif present in phospholipases, protein
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